```
                                                                  *
  Heps  RIVGGRDTSL GRWPWQVSL. ....RYDG.A HLCGGSLLSG DWVLTAAHCF PE....RNRV
Tadg15  RVVGGTDADE GEWPWQVSL. ....HALGQG HICGASLISP NWLVSAAHCY IDDRGFRYSD
  Scce  KIIDGAPCAR GSHPWQVAL. ....LSGNQL H.CGGVLVNE RWVLTAAHC. .........K
   Try  KIVGGYNCEE NSVPYQVSL. ....NSGYHF ..CGGSLINE QWVVSAGHC. .........Y
 Chymb  RIVNGEDAVP GSWPWQVSL. ....QDKTGF HFCGGSLISE DQVVTAAHC. ........GV
  Fac7  RIVGGKVCPK GECPWQVLL. ....LVNG.A QLCGGTLINT IWVVSAAHCF DKIKNWRNLI
   Tpa  RIKGGLFADI ASHPWQAAIF AKHRRSPGER FLCGGILISS CWILSAAHCF QERFPPHHL.
                                                        *
  Heps  LSRWRVFAGA VAQASPHGLQ LGVQAVVYHG GYLPFRDPNS EENSNDIALV HLSS.PLPLT
Tadg15  PTWETAFLHL HDQSQRSAPG VQERRLKRII SHPFFNDFTF D...YDIALL ELEK.FAEYS
  Scce  MNEYTVHLGS DTLG..DR.R AQRIKASKSF RHPGYSTQT. ..HVNDLMLV KLNS.QARLS
   Try  KSRIQVRLGE HNIEVLEG.N EQFINAAKII RHPQYDRKT. ..LNNDIMLI KLSS.RAVIN
 Chymb  RTSDVVVAGE FDQGSDEE.N IQVLKIAKVF KNPKFSILT. ..VNNDITLL KLAT.PARFS
  Fac7  .....AVLGE HDLSEHDGDE QSRRVAQVII P....STYVP GTTNHDIALL RLHQ.PVVLT
   Tpa  ....TVILGR .TYRVVPGEE EQKFEVEKYI VHKEFDDDTY D...NDIALL QLKSDSSRCA

  Heps  EYIQPVCLPA ...AGQALVD GKICTVTGWG NTQYYGQQ.A GVLQEAAVPI ISNDVCNGAD
Tadg15  SMVRPICLPD ...ASHVFPA GKAIWVTGWG HTQYGGTG.A LILQKGEIRV INQTTCE..N
  Scce  SMVKKVRLPS ...RCE..PP GTTCTVSGWG TTTSPDVTFP SDLMCVDVKL ISPQDCTKV.
   Try  ARVSTISLPT ...APP..AT GTKCLISGWG NTASSGADYP DELQCLDAPV LSQAKCEAS.
 Chymb  QTVSAVCLPS ...ADDDFPA GTLCATTGWG KTKYNANKTP DKLQQAALPL LSNAECKKS.
  Fac7  DHVVPLCLPE RTFSERTLAF VRFSLVSGWG QLLDRGATAL ELMVLNVPRL NTQDCLQQSR
   Tpa  QESSVVRTVC LPPADLQLPD WTECELSGYG KHEALSPFYS ERLKEAHVRL YPSSRCTSQH
```

Fig. 1A

```
                                                  *
  Heps  FYGN..QIKP KMFCAGYPEG G......IDA CQGDSGGPFV CEDSISRTPR WRLCGIVSWG
Tadg15  LLPQ..QITP RMMCVGFLSG G......VDS CQGDSGGPL. ..SSVEADGR IFQAGVVSWG
  Scce  .YKD..LLEN SMLCAGIPDS K......KNA CNGDSGGPLV C....R.... GTLQGLVSWG
   Try  .YPG..KITS NMFCVGFLEG G......KDS CQGDSGGPVV C....M.... GQLQGVVSWG
 Chymb  .WGR..RITD VMICAG..AS G......VSS CMGDSGGPLV C....QKDGA WTLVGIVSWG
  Fac7  KVGDSPNITE YMFCAGYSDG S......KDS CKGDSGGP.. ..HATHYRGT WYLTGIVSWG
   Tpa  LLNRT..VTD NMLCAGDTRS GGPQANLHDA CQGDSGGPLV CLN....DGR MTLVGIISWG

  Heps  T.GCALAQKP GVYTKVSDFR EWIFQAIKTH SEASGXVTQL --   (SEQ ID NO: 3)
Tadg15  D.GCAQRNKP GVYTRLPLFR DWIKENTGV- ---------- --   (SEQ ID NO: 14)
  Scce  TFPCGQPNDP GVYTQVCKFT KWINDTMKKH R--------- --   (SEQ ID NO: 4)
   Try  D.GCAQKNKP GVYTKVYNYV KWIKNTIAAN S--------- --   (SEQ ID NO: 5)
 Chymb  DSTCS.TSSP GVYARVTKLI PWVQKILAAN ---------- --   (SEQ ID NO: 6)
  Fac7  Q.GCATVGHF GVYTRVSQYI EWLQKLMRSE PRPGVLLRAP FP   (SEQ ID NO: 7)
   Tpa  .LGCGQKDVP GVYTKVTNYL DWIRDNMRP- ---------- --   (SEQ ID NO: 8)
```

Fig. 1B

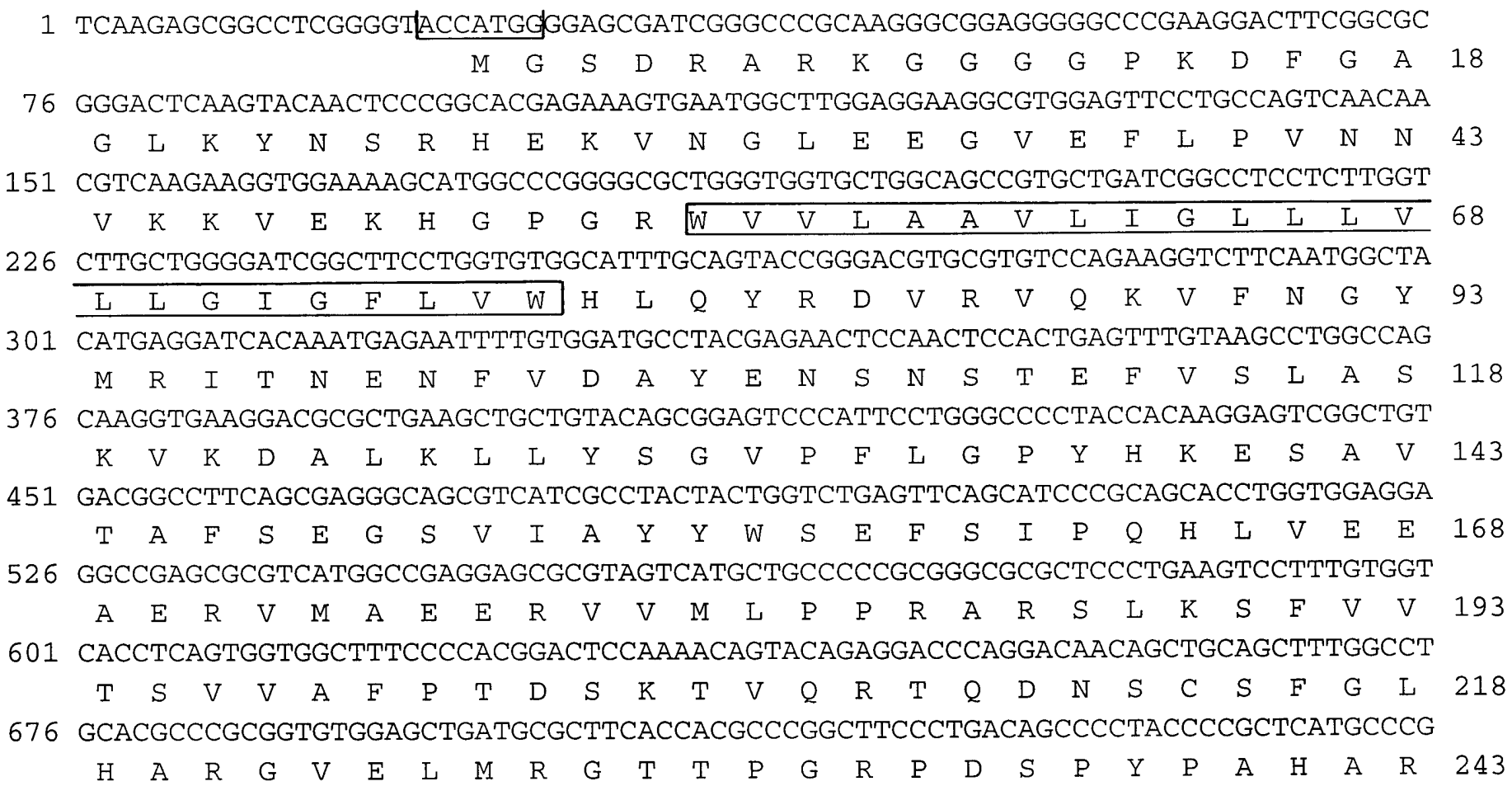

1 TCAAGAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAGGACTTCGGCGC
M G S D R A R K G G G G P K D F G A 18
76 GGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAAGGCGTGGAGTTCCTGCCAGTCAACAA
G L K Y N S R H E K V N G L E E G V E F L P V N N 43
151 CGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGT
V K K V E K H G P G R W V V L A A V L I G L L L V 68
226 CTTGCTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTA
L L G I G F L V W H L Q Y R D V R V Q K V F N G Y 93
301 CATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAG
M R I T N E N F V D A Y E N S N S T E F V S L A S 118
376 CAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTGT
K V K D A L K L L Y S G V P F L G P Y H K E S A V 143
451 GACGGCCTTCAGCGAGGGCAGCGTCATCGCCTACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGA
T A F S E G S V I A Y Y W S E F S I P Q H L V E E 168
526 GGCCGAGCGCGTCATGGCCGAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGT
A E R V M A E E R V V M L P P R A R S L K S F V V 193
601 CACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGCAGCTTTGGCCT
T S V V A F P T D S K T V Q R T Q D N S C S F G L 218
676 GCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCG
H A R G V E L M R G T T P G R P D S P Y P A H A R 243

Fig. 2A

```
751 CTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCAGTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTG
    C  Q  W  A  L  R  G  D  A  D  S  V  L  S  L  T  F  R  S  F  D  L  A  S  C  268
826 CGACGAGCGCGGCAGCGACCTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTT
    D  E  R  G  S  D  L  V  T  V  Y  N  T  L  S  P  M  E  P  H  A  L  V  Q  L  293
901 GTGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATCACACTGATAAC
    C  G  T  Y  P  P  S  Y  N  L  T  F  H  S  S  Q  N  V  L  L  I  T  L  I  T  318
976 CAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAGGATGAGCAGCTGTGGAGGCCG
    N  T  E  F  F  H  P  G  F  E  A  T  F  F  Q  L  P  R  M  S  S  C  G  G  R  343
1051 CTTACGTAAAGCCCAGGGGACATTCAACAGCCCCTACTACCCAGGCCACTACCCACCCAACATTGACTGCACATG
     L  R  K  A  Q  G  T  F  N  S  P  Y  Y  P  G  H  Y  P  P  N  I  D  C  T  W  368
1126 GAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCC
     N  I  E  V  P  N  N  Q  H  V  K  V  S  F  K  F  F  Y  L  L  E  P  G  V  P  393
1201 TGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCGT
     A  G  T  C  P  K  D  Y  V  E  I  N  G  E  K  Y  C  G  E  R  S  Q  F  V  V  418
1276 CACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTCTTAGCTGA
     T  S  N  S  N  K  I  T  V  R  F  H  S  D  Q  S  Y  T  D  T  G  F  L  A  E  443
1351 ATACCTCTCCTACGACTCCAGTGACCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGA
     Y  L  S  Y  D  S  S  D  P  C  P  G  Q  F  T  C  R  T  G  R  C  I  R  K  E  468
1426 GCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCA
     L  R  C  D  G  W  A  D  C  T  D  H  S  D  E  L  N  C  S  C  D  A  G  H  Q  493
```

Fig. 2B

```
1501 GTTCACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACAG
     F  T  C  K  N  K  F  C  K  P  L  F  W  V  C  D  S  V  N  D  C  G  D  N  S  518
1576 CGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCA
     D  E  Q  G  C  S  C  P  A  Q  T  F  R  C  S  N  G  K  C  L  S  K  S  Q  Q  543
1651 GTGCAATGGGAAGGACGACTGTGGGGACGGGTCCGACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTAC
     C  N  G  K  D  D  C  G  D  G  S  D  E  A  S  C  P  K  V  N  V  V  T  C  T  568
1726 CAAACACACCTACCGCTGCCTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTG
     K  H  T  Y  R  C  L  N  G  L  C  L  S  K  G  N  P  E  C  D  G  K  E  D  C  593
1801 TAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGGGG
     S  D  G  S  D  E  K  D  C  D  C  G  L  R  S  F  T  R  Q  A  R  V  V  G  G  618
1876 CACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGC
     T  D  A  D  E  G  E  W  P  W  Q  V  S  L  H  A  L  G  Q  G  H  I  C  G  A  643
1951 TTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGA
     S  L  I  S  P  N  W  L  V  S  A  A  H  C  Y  I  D  D  R  G  F  R  Y  S  D  668
2026 CCCCACGCAGTGGACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAG
     P  T  Q  W  T  A  F  L  G  L  H  D  Q  S  Q  R  S  A  P  G  V  Q  E  R  R  693
2101 GCTCAAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTGGA
     L  K  R  I  I  S  H  P  F  F  N  D  F  T  F  D  Y  D  I  A  L  L  E  L  E  718
2176 GAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGACGCCTCCCATGTCTTCCCTGCCGGCAA
     K  P  A  E  Y  S  S  M  V  R  P  I  C  L  P  D  A  S  H  V  F  P  A  G  K  743
```

Fig. 2C

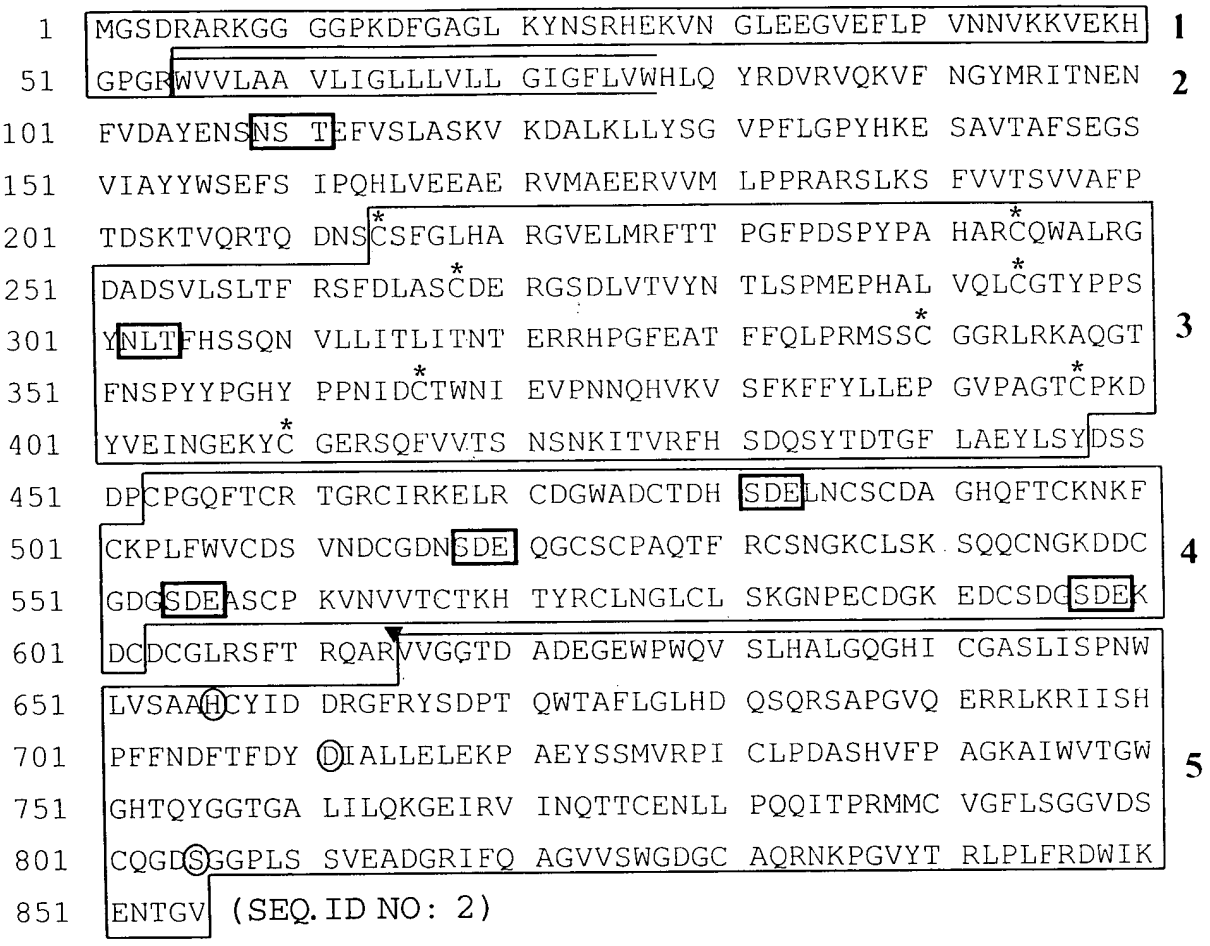
```
2251 GGCCATCTGGGTCACGGGCTGGGGACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGAT
      A  I  W  V  T  G  W  G  H  T  Q  Y  G  G  T  G  A  L  I  L  Q  K  G  E  I  768
2326 CCGCGTCATCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTT
      R  V  I  N  Q  T  T  C  E  N  L  L  P  Q  Q  I  T  P  R  M  M  C  V  G  F  793
2401 CCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGGAT
      L  S  G  G  V  D  S  C  Q  G  D  (S) G  G  P  L  S  S  V  E  A  D  G  R  I  818
2476 CTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCC
      F  Q  A  F  C  C  S  W  G  D  G  C  A  Q  R  N  K  P  G  V  Y  T  R  L  P  843
2551 TCTGTTTCGGGACTGGATCAAAGAGAACACTGGGGTATAGGGGCCGGGGCCACCCAAATGTGTACACCTGCGGGG
      L  F  R  D  W  I  K  E  N  T  G  V              (SEQ ID NO: 2)                855
2626 CCACCCATCGTCCACCCCAGTGTGCACGCCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCCCCAGAA
2701 CATACACTGTGAACTCAATCTCCAGGGCTCCAAATCTGCCTAGAAAACCTCTCGCTTCCTCAGCCTCCAAAGTGG
2776 AGCTGGGAGGTAGAAGGGGAGGACACTGGTGGTTCTACTGACCCAACTGGGGGCAAAGGTTTGAAGACACAGCCT
2851 CCCCCGCCAGCCCCAAGCTGGGCCGAGGCGCGTTTGTGTATATCTGCCTCCCCTGTCTGTAAGGAGCAGCGGGAA
2926 CGGAGCTTCGGAGCCTCCTCAGTGAAGGTGGTGGGGCTGCCGGATCTGGGCTGTGGGGCCCTTGGGCCACGCTCT
3001 TGAGGAAGCCCAGGCTCGGAGGACCCTGGAAAACAGACGGGTCTGAGACTGAAATTGTTTTACCAGCTCCCAGGG
3076 TGGACTTCAGTGTGTGTATTTGTGTAAATGGGTAAAACAATTTATTTCTTTTTAAAAAAAAAAAAAAAAAA
                                                          (SEQ ID NO: 1)
```

: KOZAK'S CONSENSUS SEQUENCE

: TRANSMEMBRANE DOMAIN

: CONSERVED AMINO ACIDS OF CATALYTIC TRIAD H,D,S

Fig. 2D



* : **Conserved cysteine residue**

NXT : **Possible N-linked glycosylation site**

SDE : **Conserved SDE motif**

▼ : **Potential cleavage site**

O : **Conserved amino acids of catalytic triad H, D, S**

1. **Cytoplasmic domain**
2. **Transmembrane domain**
3. **CUB repeat**
4. **Ligand-binding repeat (class A motif) of LDL receptor like domain**
5. **Serine protease**

Fig. 3

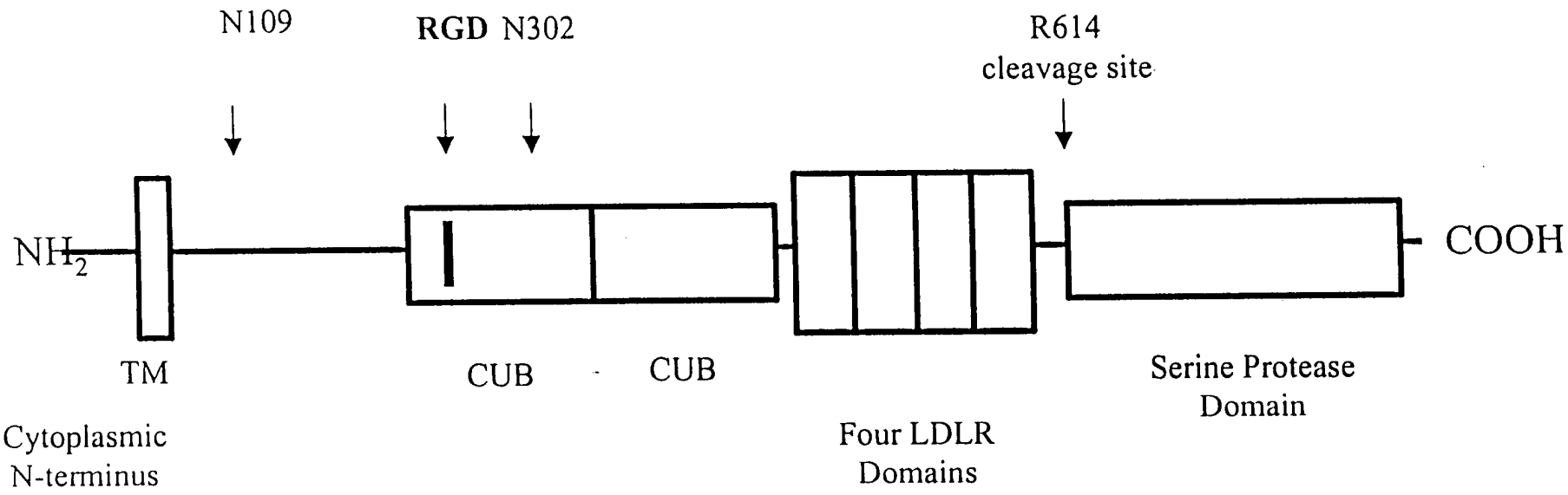

N109
RGD N302
R614
cleavage site
NH2
COOH
TM
CUB
CUB
Serine Protease
Domain
Cytoplasmic
N-terminus
Four LDLR
Domains

Fig. 4

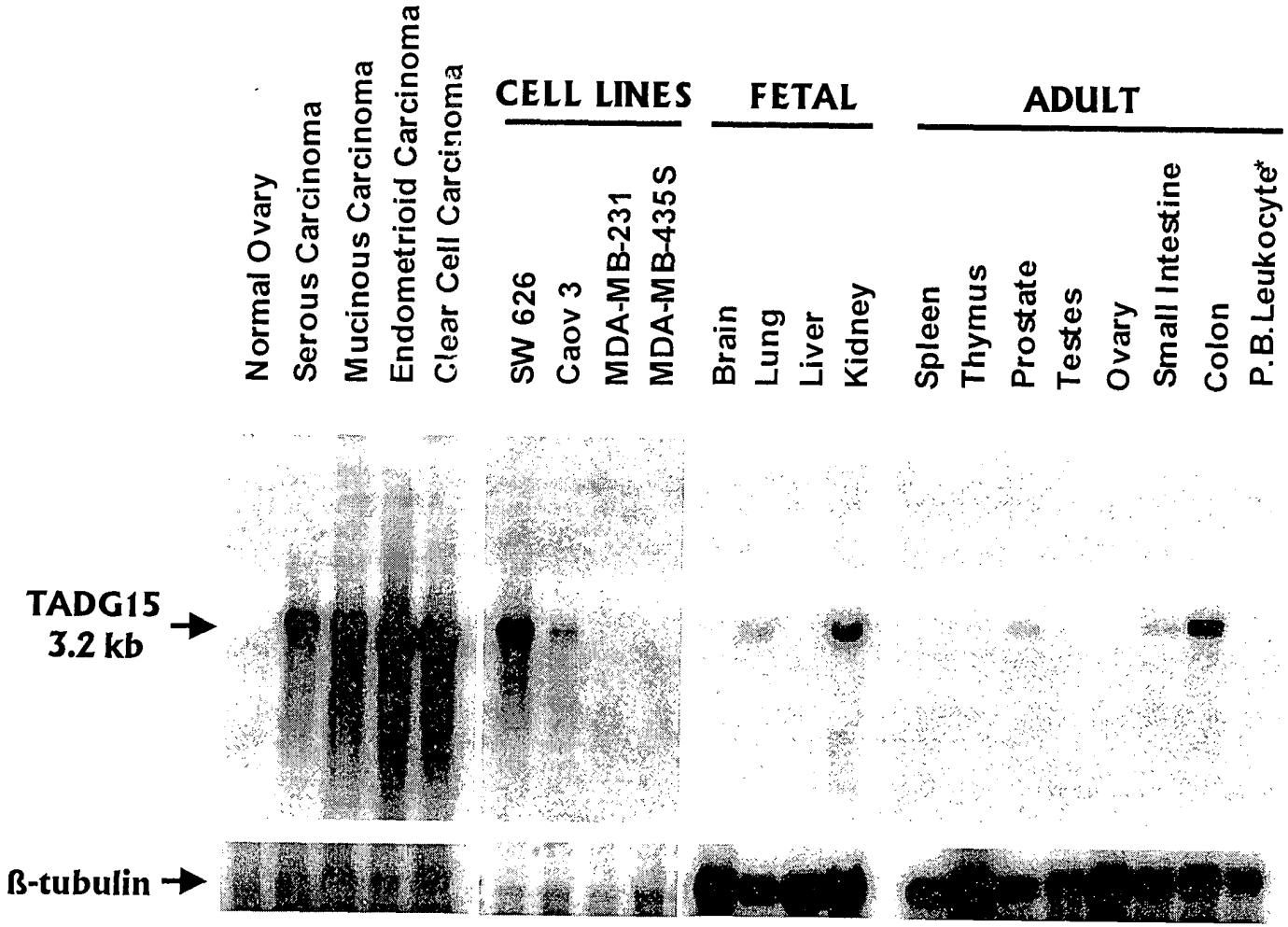

Normal Ovary
Serous Carcinoma
Mucinous Carcinoma
Endometrioid Carcinoma
Clear Cell Carcinoma
CELL LINES
SW 626
Caov 3
MDA-MB-231
MDA-MB-435S
FETAL
Brain
Lung
Liver
Kidney
ADULT
Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
P.B.Leukocyte*
TADG15
3.2 kb
ß-tubulin
* P.B. : Peripheral Blood

Fig. 5

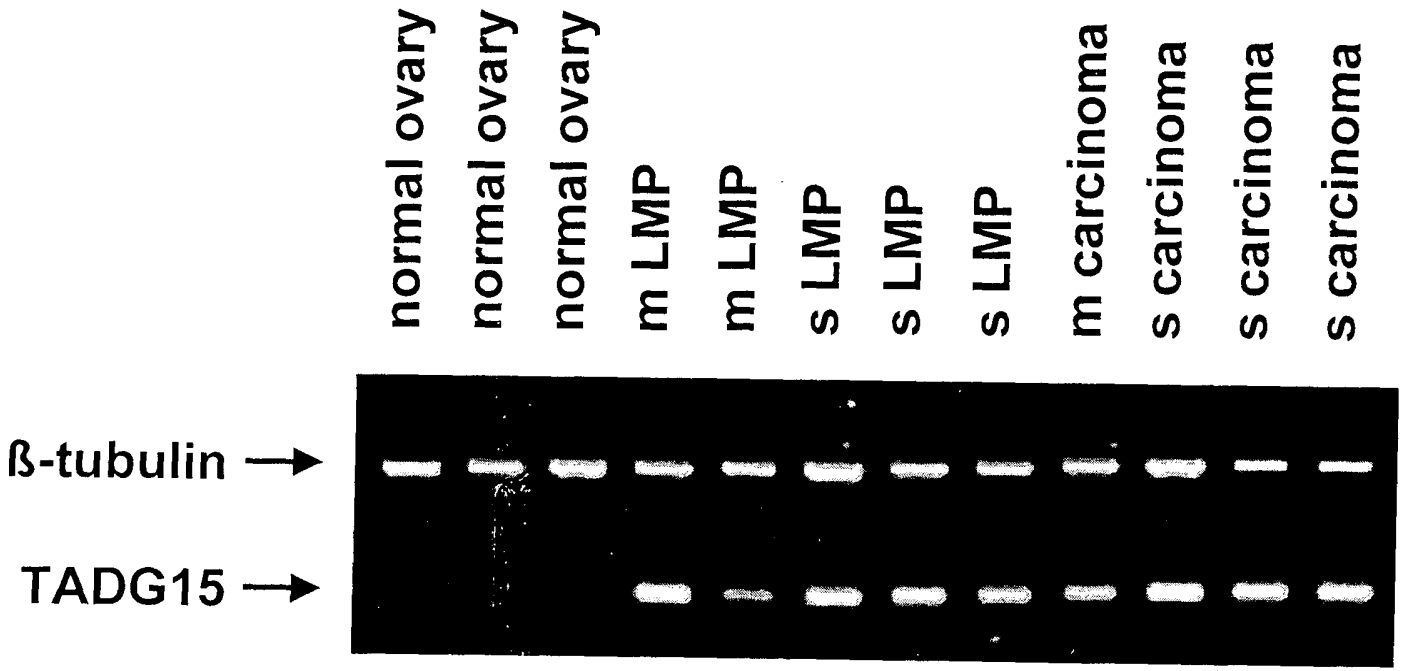

normal ovary
normal ovary
normal ovary
m LMP
m LMP
s LMP
s LMP
s LMP
m carcinoma
s carcinoma
s carcinoma
s carcinoma
ß-tubulin
TADG15

Fig. 6A

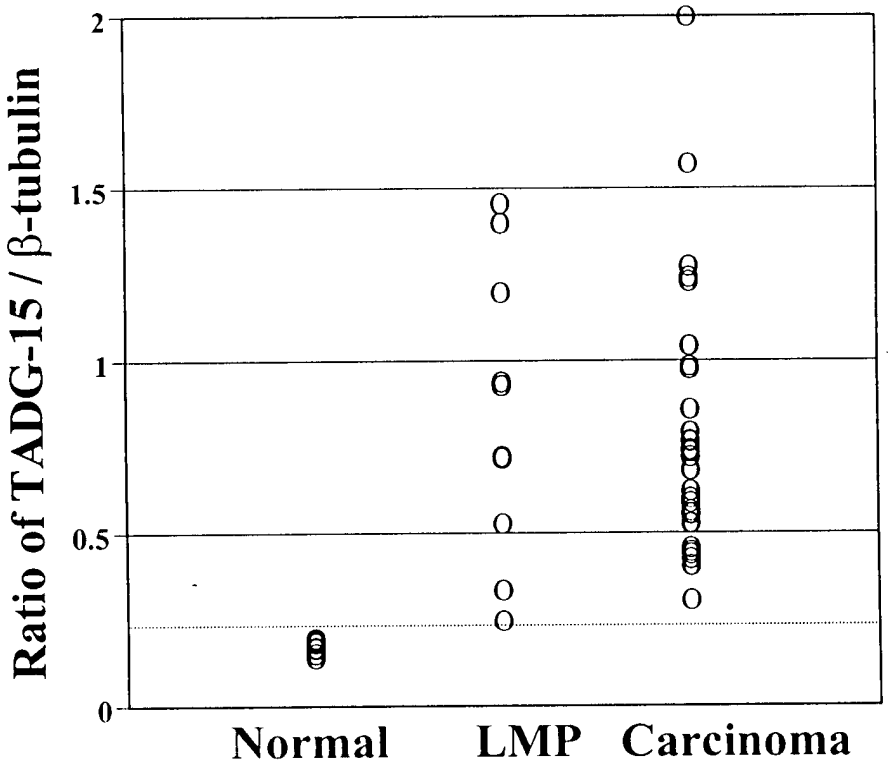


Fig. 6B

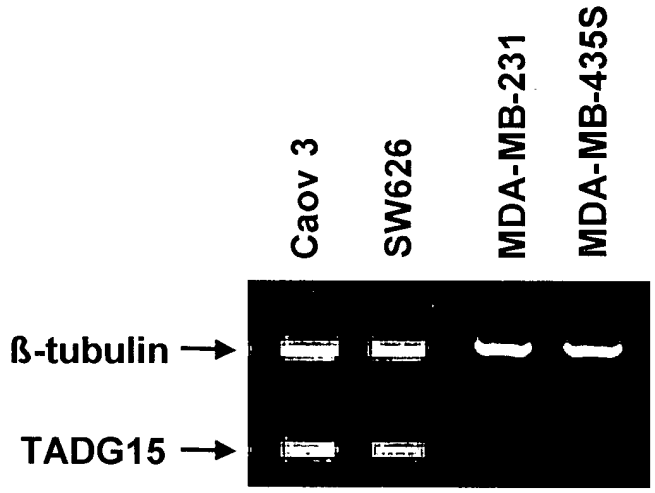

Caov 3
SW626
MDA-MB-231
MDA-MB-435S
ß-tubulin
TADG15

Fig. 7

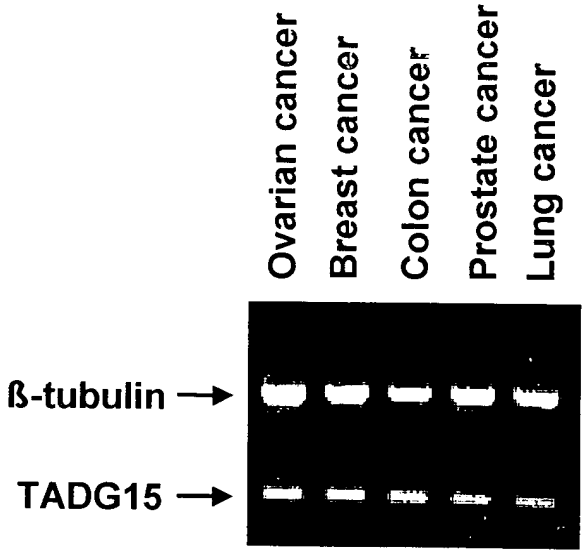

Ovarian cancer
Breast cancer
Colon cancer
Prostate cancer
Lung cancer
ß-tubulin
TADG15

Fig. 8

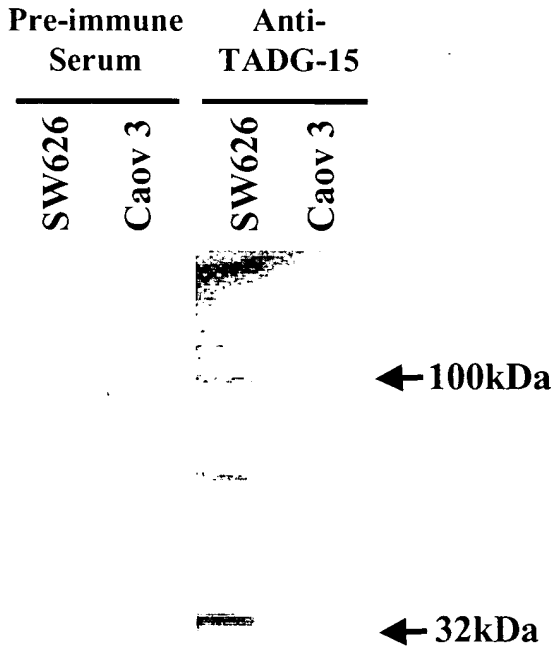

Pre-immune Serum
Anti-TADG-15
SW626
Caov 3
SW626
Caov 3
100kDa
32kDa

Fig. 9

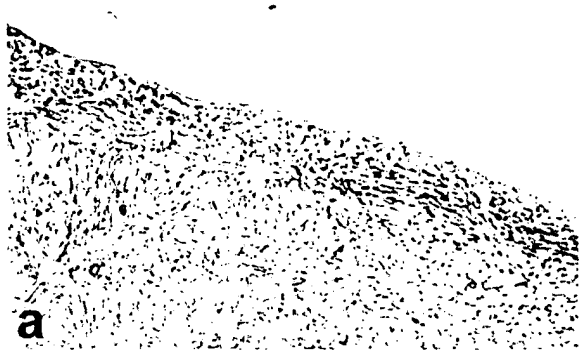


Fig. 10A

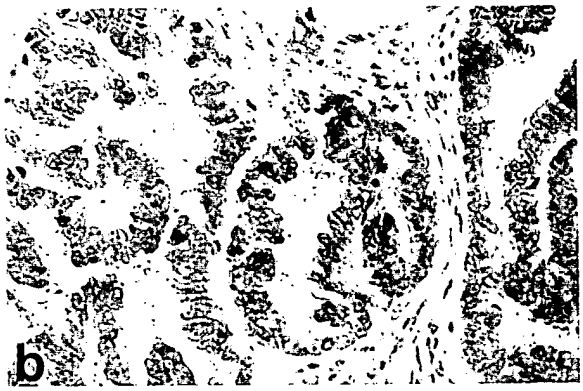


Fig. 10B

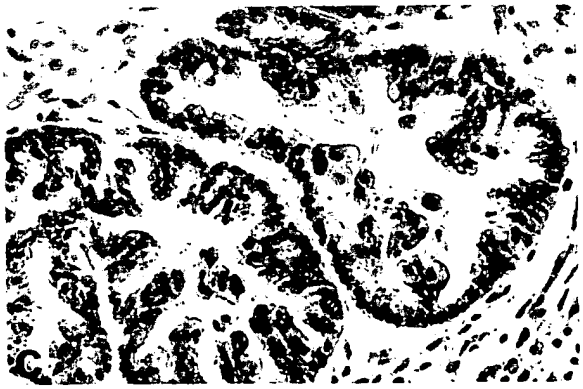


Fig. 10C

Fig. 10D

Fig. 10E

```
 hTADG15  MGSDRARKGG GGPKDFGAGL KYNSRHEKVN GLEEGVEFLP VNNVKKVEKH  50
mEpithin  ---N-G--A- --SQ------ --D--L-NM- -F-------- A--A-----R

 hTADG15  GPGRWVVLAA VLIGLLLVLL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN 100
mEpithin  --R-----V- --FSF--LS- MA-L----FH --N------- --HL-----I

 hTADG15  FVDAYENSNS TEFVSLASKV KDALKLLYSG VPFLGPYHKE SAVTAFSEGS 150
mEpithin  -L------T- ---I----Q- -E------NE --V------K ----------

 hTADG15  VIAYYWSEFS IPQHLVEEAE RVMAEERVVM LPPRARSLKS FVVTSVVAFP 200
mEpithin  ---------- --P--A--VD -A--V----T ------A--- --L-------

 hTADG15  TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG 250
mEpithin  I-PRML---- ------A--- H-AAVT---- ----N----- ------V---

 hTADG15  DADSVLSLTF RSFDLASCDE RGSDLVTVYN TLSPMEPHAL VQLCGTYPPS 300
mEpithin  ---------- ----V-P--- H--------D S--------V -R----FS--

 hTADG15  YNLTFHSSQN VLLITLITNT ERRHPGFEAT FFQLPRMSSC GGRLRKAQGT 350
mEpithin  -----L---- -F-V------ G---L----- -----K---- --V-SDT---

 hTADG15  FNSPYYPGHY PPNIDCTWNI EVPNNQHVKV SFKFFYLLEP GVPAGTCPKD 400
mEpithin  -S-------- ----N----- K----RN--- R--L---VD- N--V-S-T--

 hTADG15  YVEINGEKYC GERSQFVVTS NSNKITVRFH SDQSYTDTGF LAEYLSYDSS 450
mEpithin  --------GS --------S- --S----H-- --H------- ---------N
```

Fig. 11A

```
 hTADG15  DPCPGQFTCR TGRCIRKELR CDGWADCTDH SDELNCSCDA GHQFTCKNKF 500
mEpithin  -----M-M-K ---------- -------P-Y ---RY-R-N- T-------Q-

 hTADG15  CKPLFWVCDS VNDCGDNSDE QGCSCPAQTF RCSNGKCLSK SQQCNGKDDC 550
mEpithin  ---------- ------G--- E------GS- K-------PQ --K-----N-

 hTADG15  GDGSDEASCP KVNVVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSDEK 600
mEpithin  ---------D S----S---Y ----Q----- ---------- T---------

 hTADG15  DCDCGLRSFT RQARVVGGTD ADEGEWPWQV SLHALGQGHI CGASLISPNW 650
mEpithin  N--------- K--------N ---------- ---------L --------D-

 hTADG15  LVSAAHCYID DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH 700
mEpithin  -------FQ- -KN-K---Y- M-------L- --K---S--- -LK-----T-

 hTADG15  PFFNDFTFDY DIALLELEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGW 750
mEpithin  -S-------- ---------S V---TV---- -----T---- ----------

 hTADG15  GHTQYGGTGA LILQKGEIRV INQTTCENLL PQQITPRMMC VGFLSGGVDS 800
mEpithin  ---KE----- ---------- -------D-M ---------- ----------

 hTADG15  CQGDSGGPLS SVEADGRIFQ AGVVSWGDGC AQRNKPGVYT RLPLFRDWIK 850
mEpithin  ---------- -A-K---M-- -------E-- ---------- ---CSSGLDQ

 hTADG15  ENTGV*                                                  900
mEpithin  RAHWGIAAWT DSRPQTPTGM PDMHTWIQER NTDDIYAVAS PPQHNPDCEL

 hTADG15     SEQ ID NO: 2                                        902
mEpithin  HP SEQ ID NO: 10
```

Fig. 11B

```
            TADG15:  TCAAGAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAGGACTTCGGCGCGGGACT 81

            SNC19:   ..............................................................................

 82 CAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAAGGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGG

    ..............................................................................................

182 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGTTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 281
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 100

282 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 381
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 200

382 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 481
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 300

482 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCCGAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCT 581
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTTGAGGAGGCCGAGCGCGTCATGGCC.AGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCT 399

582 CCCTGAAGTCCTTTGTGGTCACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGACCACCCAGGACAACAGCTGCAGCTTTGGCCTGCACGC 681
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Fig. 12A

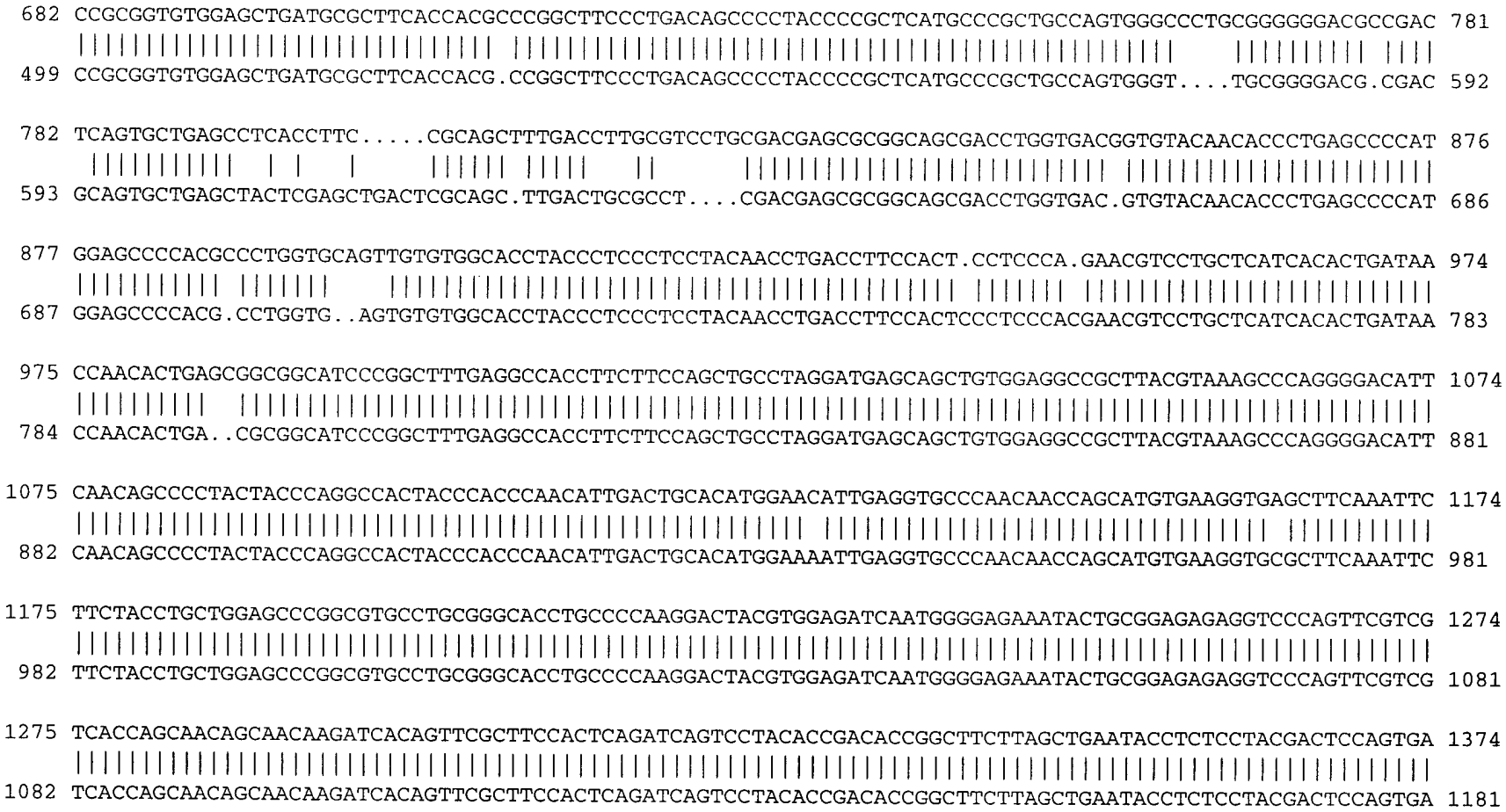
682 CCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGAC 781
499 CCGCGGTGTGGAGCTGATGCGCTTCACCACG.CCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGT....TGCGGGGACG.CGAC 592
782 TCAGTGCTGAGCCTCACCTTC.....CGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGACCTGGTGACGGTGTACAACACCCTGAGCCCCAT 876
593 GCAGTGCTGAGCTACTCGAGCTGACTCGCAGC.TTGACTGCGCCT....CGACGAGCGCGGCAGCGACCTGGTGAC.GTGTACAACACCCTGAGCCCCAT 686
877 GGAGCCCCACGCCCTGGTGCAGTTGTGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACT.CCTCCCA.GAACGTCCTGCTCATCACACTGATAA 974
687 GGAGCCCCACG.CCTGGTG..AGTGTGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCCTCCCACGAACGTCCTGCTCATCACACTGATAA 783
975 CCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATT 1074
784 CCAACACTGA..CGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATT 881
1075 CAACAGCCCCTACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGAGCTTCAAATTC 1174
882 CAACAGCCCCTACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAAAATTGAGGTGCCCAACAACCAGCATGTGAAGGTGCGCTTCAAATTC 981
1175 TTCTACCTGCTGGAGCCCGGCGTGCCTGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1274
982 TTCTACCTGCTGGAGCCCGGCGTGCCTGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1081
1275 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1374
1082 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1181

Fig. 12B

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1375 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTC 1474
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
1182 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGG.CGACTGCACCGACCACAGCGATGAGCTC 1290

1475 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACA 1574
     |||||||||||||||||||||||||||||||||||||||| ||||||||||||   |||||||||||||||||||||||||||||| ||||||||||||
1281 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAGCAAGTTCTGCAAG...CTCTTCTGGGTCTGCGACAGTGTGAACGAGTGCGGAGACAACA 1377

1575 GCGACGAGCAGGGGTGCAGTTGTCCGG.CCCAGACCTTCAGGTGTTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTG 1673
     |||||||||||| |||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1378 GCGACGAGCAGGGTTGCATTTGTCCGGACCCAGACCTTCAGGTGTTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTG 1477

1674 GGGACGGGTCCGACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1773
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1478 GGGACGGGTCCGACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1577

1774 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGG 1873
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1578 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGG 1677

1874 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1973
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1678 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1777

1974 TGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCG 2073
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
1778 TGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCA..GGACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCG 1875
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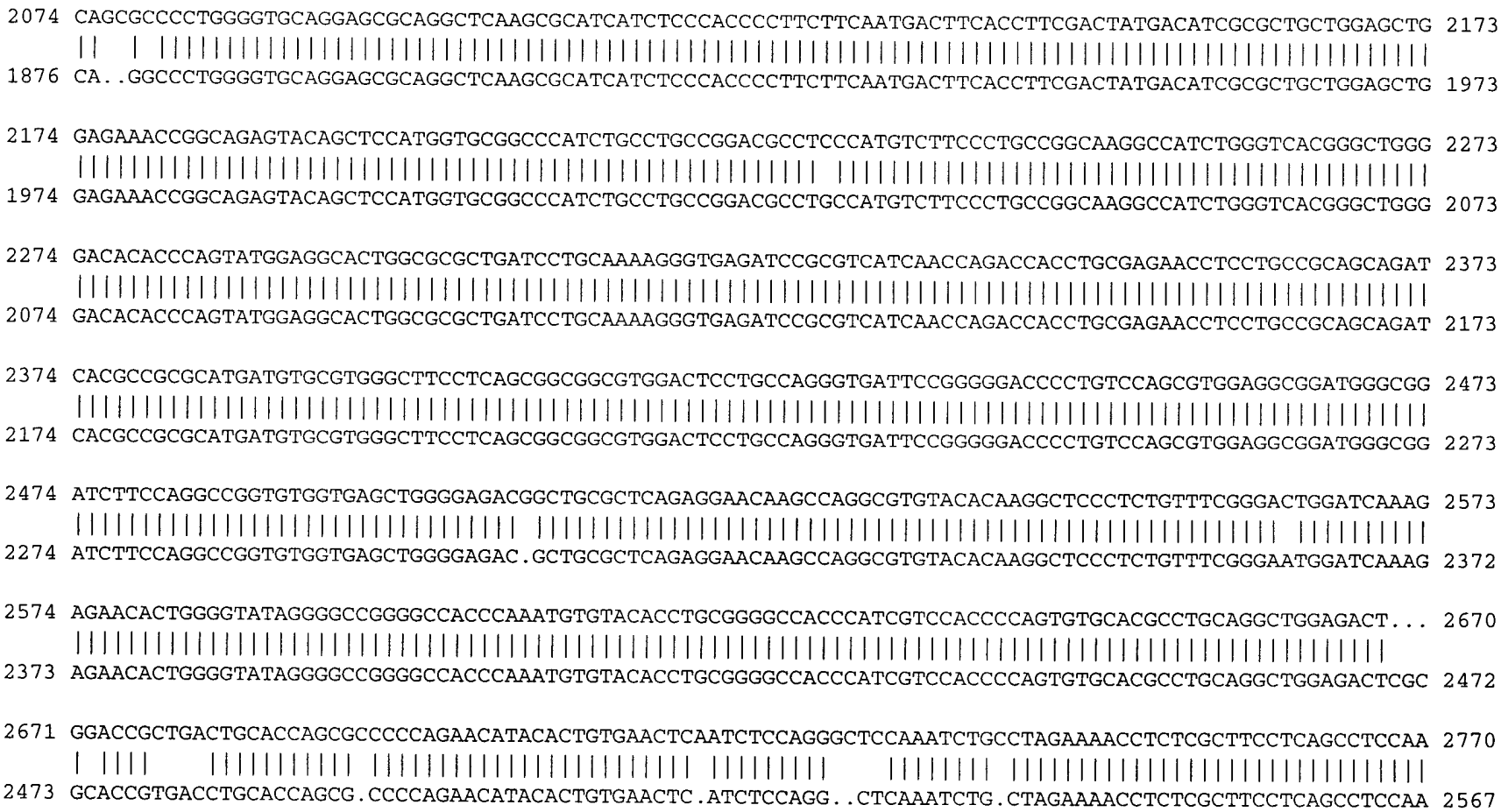
Fig. 12C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1876 CA..GGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 1973
2174 GAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGACGCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGG 2273
1974 GAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGACGCCTGCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGG 2073
2274 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGAT 2373
2074 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGAT 2173
2374 CACGCCGCGCATGATGTGCGTGGGCTTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGG 2473
2174 CACGCCGCGCATGATGTGCGTGGGCTTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGG 2273
2474 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAG 2573
2274 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGAC.GCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGAATGGATCAAAG 2372
2574 AGAACACTGGGGTATAGGGGCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCCAGTGTGCACGCCTGCAGGCTGGAGACT... 2670
2373 AGAACACTGGGGTATAGGGGCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCCAGTGTGCACGCCTGCAGGCTGGAGACTCGC 2472
2671 GGACCGCTGACTGCACCAGCGCCCCCAGAACATACACTGTGAACTCAATCTCCAGGGCTCCAAATCTGCCTAGAAAACCTCTCGCTTCCTCAGCCTCCAA 2770
2473 GCACCGTGACCTGCACCAGCG.CCCCAGAACATACACTGTGAACTC.ATCTCCAGG..CTCAAATCTG.CTAGAAAACCTCTCGCTTCCTCAGCCTCCAA 2567

Fig. 12D

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2771 AGTGGAGCTGGGA.GGTAGAAGGGGAGG.ACACTGGTGGTTCTACTGACCCAACTGGGGGCAAAGGTTTGAAGACACAGCCTCCCCCGCCAGCCCCAAGC 2868
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2568 AGTGGAGCTGGGAGGGTAGAAGGGGAGGAACACTGGTGGTTCTACTGACCCAACTGGGG..CAAGGTTTGAAG.CACAG....CTCCGGCAGCCC..AAG 2658

2869 TGGGCCGAGGCGCGTTTGTGTATATCTGCCTCCCCTGTCTGTAAGGAGCAGCGGGAACGGAGCTTCGGAGCCTCCTCAGTGAAGGTGGTGGGGCTGCCGG 2968
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2659 TGGGCGAGGACGCGTTTGTGCATA.CTGCC.CTGCTCTATACACGGAAGACCTGGA.............TCTCTAGTGA.....GTGTGACTGCCGG 2735

2969 ATCTGGGCTGTGGGGCCCTTGGGCCACGCTCTTGAGGAAGCCCAGGCTCGGAGGACCCTGGAAAACAGACGGGTCTGAGACTGAAATTGTTTTACCAGCT 3068
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2736 ATCTGG...CTGTGGTCCTTGGCCACGCTTCTTGAGGAAGCCCAGGCTCGGAGGACCCTGGAAAACAGACGGGTCTGAGACTGAAAATGGTTTACCAGCT 2832

3069 CCCAGGGTGGACTTCAGTGTGTGTATTTGTGTAAATGGGTAAAACAATTTATTTCTTTTTAAAAAAAAAAAAAAAAAAA 3147 (SEQ ID NO: 1)
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2833 CCCAGG..TGACTTCAGTGTGTGTA.TTGTGTAAATGAGTAAAACATTTTATTTCTTTTTAAAAAAAAAAA..... 2900 (SEQ ID NO: 9)
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Fig. 12E